



#5

SEQUENCE LISTING

<110> Medlock, Eugene
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<120> IL-17 Like Molecules and Uses Thereof

<130> 01017/37128C

<140> 10/037,591

<141> 2001-12-21

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<150> 60/266,159

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<150> 60/213,125

<151> 2000-06-22

<160> 24

<170> PatentIn Ver. 2.0

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<222> (159)..(641)

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tcagtgcgcc acttggtgact gagtgtgcag tgcccagc atg tac cag gtg gtt gca 176
Met Tyr Gln Val Val Ala

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ttc ttg gca atg gtc atg gga acc cac acc tac agc cac tgg ccc agc 224
Phe Leu Ala Met Val Met Gly Thr His Thr Tyr Ser His Trp Pro Ser

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tgc tgc ccc agc aaa ggg cag gac acc tct gag gag ctg ctg agg tgg 272
Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser Glu Glu Leu Leu Arg Trp

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agc act gtg cct gtg cct ccc cta gag cct gct agg ccc aac cgc cac 320
Ser Thr Val Pro Val Pro Pro Leu Glu Pro Ala Arg Pro Asn Arg His

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cca gag tcc tgt agg gcc agt gaa gat gga ccc ctc aac agc agg gcc	368
Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly Pro Leu Asn Ser Arg Ala	
55 60 65 70	
atc tcc ccc tgg aga tat gag ttg gac aga gac ttg aac cgg ctc ccc	416
Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg Asp Leu Asn Arg Leu Pro	
75 80 85	
cag gac ctg tac cac gcc cgt tgc ctg tgc ccg cac tgc gtc agc cta	464
Gln Asp Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu	
90 95 100	
cag aca ggc tcc cac atg gac ccc cgg ggc aac tcg gag ctg ctc tac	512
Gln Thr Gly Ser His Met Asp Pro Arg Gly Asn Ser Glu Leu Leu Tyr	
105 110 115	
cac aac cag act gtc ttc tac cgg cgg cca tgc cat ggc gag aag ggc	560
His Asn Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Lys Gly	
120 125 130	
acc cac aag ggc tac tgc ctg gag cgc agg ctg tac cgt gtt tcc tta	608
Thr His Lys Gly Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu	
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155 160	

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 <213> Homo sapiens

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 Glu Glu Leu Leu Arg Trp Ser Thr Val Pro Val Pro Pro Leu Glu Pro
 35 40 45
 Ala Arg Pro Asn Arg His Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly
 50 55 60
 Pro Leu Asn Ser Arg Ala Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg
 65 70 75 80
 Asp Leu Asn Arg Leu Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys
 85 90 95
 Pro His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Arg Gly
 100 105 110
 Asn Ser Glu Leu Leu Tyr His Asn Gln Thr Val Phe Tyr Arg Arg Pro
 115 120 125
 Cys His Gly Glu Lys Gly Thr His Lys Gly Tyr Cys Leu Glu Arg Arg
 130 135 140

Leu Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg Val Met
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<220>
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 <222> (1)..(507)

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 gtc agc ttg cgg atc cag gag ggc tgc agt cac ttg ccc agc tgc tgc 96
 Val Ser Leu Arg Ile Gln Glu Gly Cys Ser His Leu Pro Ser Cys Cys
 20 25 30
 ccc agc aaa gag caa gaa ccc ccg gag gag tgg ctg aag tgg agc tct 144
 Pro Ser Lys Glu Gln Glu Pro Pro Glu Glu Trp Leu Lys Trp Ser Ser
 35 40 45
 gca tct gtg tcc ccc cca gag cct ctg agc cac acc cac cac gca gaa 192
 Ala Ser Val Ser Pro Pro Glu Pro Leu Ser His Thr His His Ala Glu
 50 55 60
 tcc tgc agg gcc agc aag gat ggc ccc ctc aac agc agg gcc atc tct 240
 Ser Cys Arg Ala Ser Lys Asp Gly Pro Leu Asn Ser Arg Ala Ile Ser
 65 70 75 80
 cct tgg agc tat gag ttg gac agg gac ttg aat cgg gtc ccc cag gac 288
 Pro Trp Ser Tyr Glu Leu Asp Arg Asp Leu Asn Arg Val Pro Gln Asp
 85 90 95
 ctg tac cac gct cga tgc ctg tgc cca cac tgc gtc agc cta cag aca 336
 Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu Gln Thr
 100 105 110
 ggc tcc cac atg gac ccg ctg ggc aac tcc gtc cca ctt tac cac aac 384
 Gly Ser His Met Asp Pro Leu Gly Asn Ser Val Pro Leu Tyr His Asn
 115 120 125
 cag acg gtc ttc tac cgg cgg cca tgc cat ggc gag gaa ggt acc cat 432
 Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Glu Gly Thr His
 130 135 140
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 Arg Arg Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu Ala Cys
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 Val Cys Val Arg Pro Arg Val Met Ala
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 aaaaaa 1013

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 Pro Ser Lys Glu Gln Glu Pro Pro Glu Glu Trp Leu Lys Trp Ser Ser
 35 40 45
 Ala Ser Val Ser Pro Pro Glu Pro Leu Ser His Thr His His Ala Glu
 50 55 60
 Ser Cys Arg Ala Ser Lys Asp Gly Pro Leu Asn Ser Arg Ala Ile Ser
 65 70 75 80
 Pro Trp Ser Tyr Glu Leu Asp Arg Asp Leu Asn Arg Val Pro Gln Asp
 85 90 95
 Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu Gln Thr
 100 105 110
 Gly Ser His Met Asp Pro Leu Gly Asn Ser Val Pro Leu Tyr His Asn
 115 120 125
 Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Glu Gly Thr His
 130 135 140
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 145 150 155 160
 Val Cys Val Arg Pro Arg Val Met Ala
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<210> 5
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 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn
 35 40 45
 Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser
 50 55 60
 Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu
 65 70 75 80
 Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His
 85 90 95
 Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser
 100 105 110
 Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His
 115 120 125
 Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys
 130 135 140
 Thr Cys Val Thr Pro Ile Val His His Val Ala
 145 150 155

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 <213> Homo sapiens

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 Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg
 35 40 45
 Ile Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val
 50 55 60
 Asn Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val
 65 70 75 80
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 Thr Gly Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Val Ala Gly
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 Cys Thr Cys Ile Phe
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<213> Homo sapiens

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Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg
35 40 45

Ile Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val
50 55 60

Asn Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val
65 70 75 80

Phe Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg
85 90 95

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100 105 110

Cys Thr Cys Ile Phe
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<210> 8

<211> 197

<212> PRT

<213> Homo sapiens

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35 40 45

Pro His Leu Leu Ala Arg Gly Ala Lys Trp Gly Gln Ala Leu Pro Val
50 55 60

Ala Leu Val Ser Ser Leu Glu Ala Ala Ser His Arg Gly Arg His Glu
65 70 75 80

Arg Pro Ser Ala Thr Thr Gln Cys Pro Val Leu Arg Pro Glu Glu Val
85 90 95

Leu Glu Ala Asp Thr His Gln Arg Ser Ile Ser Pro Trp Arg Tyr Arg
100 105 110

Val Asp Thr Asp Glu Asp Arg Tyr Pro Gln Lys Leu Ala Phe Ala Glu
115 120 125

Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu Thr Ala
130 135 140

Ala Leu Asn Ser Val Arg Leu Leu Gln Ser Leu Leu Val Leu Arg Arg
 145 150 155 160

Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly Ala Phe
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Ala Phe His Thr Glu Phe Ile His Val Pro Val Gly Cys Thr Cys Val
 180 185 190

Leu Pro Arg Ser Val
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 gcctaggggtc gagggccatt atcacctaca aatcagaatg tgggagtgct attctagagg 180
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 Met Ile Val Gly Thr His Thr Val
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 Ser Leu Arg Ile Gln Glu Gly Cys Ser His Leu Pro Ser Cys Cys Pro
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 25 30 35 40

tct gtg tcc ccc cca gag cct ctg agc cac acc cac cac gca gaa tcc 678
 Ser Val Ser Pro Pro Glu Pro Leu Ser His Thr His His Ala Glu Ser
 45 50 55

tgc agg gcc agc aag gat ggc ccc ctc aac agc agg gcc atc tct cct 726
 Cys Arg Ala Ser Lys Asp Gly Pro Leu Asn Ser Arg Ala Ile Ser Pro
 60 65 70

tgg agc tat gag ttg gac agg gac ttg aat cgg gtc ccc cag gac ctg 774
 Trp Ser Tyr Glu Leu Asp Arg Asp Leu Asn Arg Val Pro Gln Asp Leu
 75 80 85

tac cac gct cga tgc ctg tgc cca cac tgc gtc agc cta cag aca ggc 822
 Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu Gln Thr Gly
 90 95 100
 tcc cac atg gac ccg ctg ggc aac tcc gtc cca ctt tac cac aac cag 870
 Ser His Met Asp Pro Leu Gly Asn Ser Val Pro Leu Tyr His Asn Gln
 105 110 115 120
 acg gtc ttc tac cgg cgg cca tgc cat ggc gag gaa ggt acc cat cgc 918
 Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Glu Gly Thr His Arg
 125 130 135
 cgc tac tgc ttg gag cgc agg ctc tac cga gtc tcc ttg gct tgt gtg 966
 Arg Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu Ala Cys Val
 140 145 150
 tgt gtg cgg ccc cgg gtc atg gcttagtcat gctcaccacc tgcctgaggc 1017
 Cys Val Arg Pro Arg Val Met
 155
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 tgcagccagg tgtaattgcc ttgaaggatg gttctgaggt gaaagctggt atcgaaaagt 1437
 aagagattta tccaaataaa catctgtgtt taataaaaaa aaaaaaaaaa aaaaaaaaaa 1496

<210> 10
 <211> 159
 <212> PRT
 <213> Mus musculus

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 Glu Trp Leu Lys Trp Ser Ser Ala Ser Val Ser Pro Pro Glu Pro Leu
 35 40 45
 Ser His Thr His His Ala Glu Ser Cys Arg Ala Ser Lys Asp Gly Pro
 50 55 60
 Leu Asn Ser Arg Ala Ile Ser Pro Trp Ser Tyr Glu Leu Asp Arg Asp
 65 70 75 80
 Leu Asn Arg Val Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys Pro
 85 90 95

His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Leu Gly Asn
 100 105 110

Ser Val Pro Leu Tyr His Asn Gln Thr Val Phe Tyr Arg Arg Pro Cys
 115 120 125

His Gly Glu Glu Gly Thr His Arg Arg Tyr Cys Leu Glu Arg Arg Leu
 130 135 140

Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg Val Met
 145 150 155

<210> 11
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Epogen signal
 peptide

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 1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly
 20 25

<210> 12
 <211> 233
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide of Fc
 fragment

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 Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
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Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160
 Asp Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 165 170 175
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 180 185 190
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 195 200 205
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 210 215 220
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 13
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Peptide of HIV
 TAT protein

<400> 13
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 1 5 10

<210> 14
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Peptide of HIV
 TAT protein

<400> 14
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Arg Arg Arg

<210> 15
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 15
tagggccagt gaagatgg 18

<210> 16
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 16
tacagcctgc gctccaggca gtagcc 26

<210> 17
<211> 1841
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (50)..(1555)

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Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val Pro Arg Glu
5 10 15

ccg acc gtt caa tgt ggc tct gaa act ggg cca tct cca gag tgg atg 154
Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro Glu Trp Met
20 25 30 35

cta caa cat gat cta atc ccc gga gac ttg agg gac ctc cga gta gaa 202
Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu Arg Val Glu
40 45 50

cct gtt aca act agt gtt gca aca ggg gac tat tca att ttg atg aat 250
Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile Leu Met Asn
55 60 65

gta agc tgg gta ctc cgg gca gat gcc agc atc cgc ttg ttg aag gcc 298
Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu Leu Lys Ala
70 75 80

acc aag att tgt gtg acg ggc aaa agc aac ttc cag tcc tac agc tgt 346
Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser Tyr Ser Cys
85 90 95

gtg agg tgc aat tac aca gag gcc ttc cag act cag acc aga ccc tct 394
Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr Arg Pro Ser
100 105 110 115

ggt ggt aaa tgg aca ttt tcc tac atc ggc ttc cct gta gag ctg aac 442
Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn
120 125 130

aca gtc tat ttc att ggg gcc cat aat att cct aat gca aat atg aat 490
Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn
135 140 145

gaa gat ggc cct tcc atg tct gtg aat ttc acc tca cca ggc tgc cta 538
Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu
150 155 160

gac cac ata atg aaa tat aaa aaa aag tgt gtc aag gcc gga agc ctg 586
Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu
165 170 175

tgg gat ccg aac atc act gct tgt aag aag aat gag gag aca gta gaa 634
Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu
180 185 190 195

gtg aac ttc aca acc act ccc ctg gga aac aga tac atg gct ctt atc 682
Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile
200 205 210

caa cac agc act atc atc ggg ttt tct cag gtg ttt gag cca cac cag 730
Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln
215 220 225

aag aaa caa acg cga gct tca gtg gtg att cca gtg act ggg gat agt 778
Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser
230 235 240

gaa ggt gct acg gtg cag ctg act cca tat ttt cct act tgt ggc agc 826
Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser
245 250 255

gac tgc atc cga cat aaa gga aca gtt gtg ctc tgc cca caa aca ggc 874
Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly
260 265 270 275

gtc cct ttc cct ctg gat aac aac aaa agc aag ccg gga ggc tgg ctg 922
Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu
280 285 290

cct ctc ctc ctg ctg tct ctg ctg gtg gcc aca tgg gtg ctg gtg gca 970
Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala
295 300 305

ggg atc tat cta atg tgg agg cac gaa agg atc aag aag act tcc ttt 1018
Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe
310 315 320

tct acc acc aca cta ctg ccc ccc att aag gtt ctt gtg gtt tac cca 1066
Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro
325 330 335

tct gaa ata tgt ttc cat cac aca att tgt tac ttc act gaa ttt ctt 1114
Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu
340 345 350 355

caa aac cat tgc aga agt gag gtc atc ctc gaa aag tgg cag aaa aag 1162
Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys
360 365 370

aaa ata gca gag atg ggt cca gtg cag tgg ctt gcc act caa aag aag 1210
Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys
375 380 385

gca gca gac aaa gtc gtc ttc ctt tcc aat gac gtc aac agt gtg 1258
Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val
390 395 400

tgc gat ggt acc tgt ggc aag agc gag ggc agt ccc agt gag aac tct 1306
Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser
405 410 415

caa gac ctc ttc ccc ctt gcc ttt aac ctt ttc tgc agt gat cta aga 1354
Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg
420 425 430 435

agc cag att cat ctg cac aaa tac gtg gtg gtc tac ttt aga gag att 1402
Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile
440 445 450

gat aca aaa gac gat tac aat gct ctc agt gtc tgc ccc aag tac cac 1450
Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His
455 460 465

ctc atg aag gat gcc act gct ttc tgt gca gaa ctt ctc cat gtc aag 1498
Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys
470 475 480

cag cag gtg tca gca gga aaa aga tca caa gcc tgc cac gat ggc tgc 1546
Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys
485 490 495

tgc tcc ttg tagccccaccc atgagaagca agagacctta aaggcttcct 1595
Cys Ser Leu
500

atccccaccaa ttacagggaa aaaacgtgtg atgatacctga agcttactat gcagcctaca 1655

aacagcctta gtaattaaaa cattttatac caataaaaatt ttcaaataatt gctaactaat 1715

gtagcattaa ctaacgattg gaaactacat ttacaacttc aaagctgttt tatacataga 1775

aatcaattac agctttaatt gaaaactgta accattttga taatgcaaca ataaagcatc 1835

ttcagc 1841

<210> 18

<211> 502

<212> PRT

<213> Homo sapiens

<400> 18.

Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
1 5 10 15

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
20 25 30

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
 50 55 60
 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
 65 70 75 80
 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
 85 90 95
 Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
 100 105 110
 Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
 115 120 125
 Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
 130 135 140
 Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
 145 150 155 160
 Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
 165 170 175
 Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
 180 185 190
 Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
 195 200 205
 Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
 210 215 220
 Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
 225 230 235 240
 Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
 245 250 255
 Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
 260 265 270
 Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
 275 280 285
 Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
 290 295 300
 Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys
 305 310 315 320
 Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val
 325 330 335
 Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr
 340 345 350
 Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp
 355 360 365

Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr
 370 375 380
 Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val
 385 390 395 400
 Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser
 405 410 415
 Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser
 420 425 430
 Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe
 435 440 445
 Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro
 450 455 460
 Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
 465 470 475 480
 His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His
 485 490 495
 Asp Gly Cys Cys Ser Leu
 500

<210> 19
 <211> 2015
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
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<400> 19
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gtg ctg cta agc ctg gcc gcg ctg tgc agg agc gcc gta ccc cga gag 106
 Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val Pro Arg Glu
 5 10 15

ccg acc gtt caa tgt ggc tct gaa act ggg cca tct cca gag tgg atg 154
 Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro Glu Trp Met
 20 25 30 35

cta caa cat gat cta atc ccc gga gac ttg agg gac ctc cga gta gaa 202
 Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu Arg Val Glu
 40 45 50

cct gtt aca act agt gtt gca aca ggg gac tat tca att ttg atg aat 250
 Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile Leu Met Asn
 55 60 65

gta agc tgg gta ctc cgg gca gat gcc agc atc cgc ttg ttg aag gcc 298
 Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu Leu Lys Ala
 70 75 80

acc aag att tgt gtg acg ggc aaa agc aac ttc cag tcc tac agc tgt	346
Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser Tyr Ser Cys	
85 90 95	
gtg agg ctg gag tgc agt ggt gcg atc atg gct cgc tgc gac ctc aat	394
Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys Asp Leu Asn	
100 105 110 115	
ctt ctg ggc tca agc gat cgt tct gct tca gcc tcc cga gcg gct ggg	442
Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Ala Ser Arg Ala Ala Gly	
120 125 130	
act gca ggc gtg ggc cac cag acc tgg cta att ttt gta gtt ttt gta	490
Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val Val Phe Val	
135 140 145	
gag ggg ggt ttc acc gtg ttg ctg gtc ttg aat tcc agt gct cag gcg	538
Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser Ala Gln Ala	
150 155 160	
atc tgc ctg cct cgg ctt ccc aaa gtg ctg gga tta cag tgg aca ttt	586
Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln Trp Thr Phe	
165 170 175	
tcc tac atc ggc ttc cct gta gag ctg aac aca gtc tat ttc att ggg	634
Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr Phe Ile Gly	
180 185 190 195	
gcc cat aat att cct aat gca aat atg aat gaa gat ggc cct tcc atg	682
Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly Pro Ser Met	
200 205 210	
tct gtg aat ttc acc tca cca ggc tgc cta gac cac ata atg aaa tat	730
Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile Met Lys Tyr	
215 220 225	
aaa aaa aag tgt gtc aag gcc gga agc ctg tgg gat ccg aac atc act	778
Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr	
230 235 240	
gct tgt aag aag aat gag gag aca gta gaa gtg aac ttc aca acc act	826
Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe Thr Thr Thr	
245 250 255	
ccc ctg gga aac aga tac atg gct ctt atc caa cac agc act atc atc	874
Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser Thr Ile Ile	
260 265 270 275	
ggg ttt tct cag gtg ttt gag cca cac cag aag aaa caa acg cga gct	922
Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln Thr Arg Ala	
280 285 290	
tca gtg gtg att cca gtg act ggg gat agt gaa ggt gct acg gtg cag	970
Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala Thr Val Gln	
295 300 305	
ctg act cca tat ttt cct act tgt ggc agc gac tgc atc cga cat aaa	1018
Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile Arg His Lys	
310 315 320	
gga aca gtt gtg ctc tgc cca caa aca ggc gtc cct ttc cct ctg gat	1066
Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe Pro Leu Asp	
325 330 335	

aac aac aaa agc aag ccg gga ggc tgg ctg cct ctc ctc ctg ctg tct 1114
 Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser 355
 340 345 350

ctg ctg gtg gcc aca tgg gtg ctg gtg gca ggg atc tat cta atg tgg 1162
 Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr Leu Met Trp 370
 360 365

agg cac gaa agg atc aag aag act tcc ttt tct acc acc aca cta ctg 1210
 Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu 385
 375 380

ccc ccc att aag gtt ctt gtg gtt tac cca tct gaa ata tgt ttc cat 1258
 Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile Cys Phe His 400
 390 395

cac aca att tgt tac ttc act gaa ttt ctt caa aac cat tgc aga agt 1306
 His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His Cys Arg Ser 415
 405 410

gag gtc atc ctc gaa aag tgg cag aaa aag aaa ata gca gag atg ggt 1354
 Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala Glu Met Gly 435
 420 425 430

cca gtg cag tgg ctt gcc act caa aag aag gca gca gac aaa gtc gtc 1402
 Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp Lys Val Val 450
 440 445

ttc ctt ctt tcc aat gac gtc aac agt gtg tgc gat ggt acc tgt ggc 1450
 Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly Thr Cys Gly 465
 455 460

aag agc gag ggc agt ccc agt gag aac tct caa gac ctc ttc ccc ctt 1498
 Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu 480
 470 475

gcc ttt aac ctt ttc tgc agt gat cta aga agc cag att cat ctg cac 1546
 Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile His Leu His 495
 485 490

aaa tac gtg gtg gtc tac ttt aga gag att gat aca aaa gac gat tac 1594
 Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr 515
 500 505 510

aat gct ctc agt gtc tgc ccc aag tac cac ctc atg aag gat gcc act 1642
 Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys Asp Ala Thr 530
 520 525

gct ttc tgt gca gaa ctt ctc cat gtc aag cag cag gtg tca gca gga 1690
 Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val Ser Ala Gly 545
 535 540

aaa aga tca caa gcc tgc cac gat ggc tgc tgc tcc ttg tagccccaccc 1739
 Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu 560
 550 555

atgagaagca agagacctta aaggcttcct atccccaccaa ttacagggaa aaaacgtgtg 1799

atgatcctga agcttactat gcagcctaca aacagcctta gtaattaaaa catttttatac 1859

caataaaatt ttcaaatatt gctaactaat gtagcattaa ctaacgattg gaaactacat 1919

ttacaacttc aaagctgttt tatacataga aatcaattac agctttaatt gaaaactgta 1979
accattttga taatgcaaca ataaagcatc ttcagc 2015

<210> 20
<211> 560
<212> PRT
<213> Homo sapiens

<400> 20
Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
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Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
20 25 30
Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
35 40 45
Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60
Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80
Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95
Tyr Ser Cys Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys
100 105 110
Asp Leu Asn Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Ala Ser Arg
115 120 125
Ala Ala Gly Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val
130 135 140
Val Phe Val Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser
145 150 155 160
Ala Gln Ala Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln
165 170 175
Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr
180 185 190
Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly
195 200 205
Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile
210 215 220
Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro
225 230 235 240
Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe
245 250 255
Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser
260 265 270

Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln
 275 280 285
 Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala
 290 295 300
 Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile
 305 310 315 320
 Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe
 325 330 335
 Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu
 340 345 350
 Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr
 355 360 365
 Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr
 370 375 380
 Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile
 385 390 395 400
 Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His
 405 410 415
 Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala
 420 425 430
 Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp
 435 440 445
 Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly
 450 455 460
 Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu
 465 470 475 480
 Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile
 485 490 495
 His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys
 500 505 510
 Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys
 515 520 525
 Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val
 530 535 540
 Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu
 545 550 555 560

<210> 21
 <211> 521
 <212> PRT
 <213> Homo sapiens

<400> 21
 Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
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Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
 20 25 30
 Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
 35 40 45
 Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
 50 55 60
 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
 65 70 75 80
 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
 85 90 95
 Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Ser
 100 105 110
 Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn
 115 120 125
 Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn
 130 135 140
 Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu
 145 150 155 160
 Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu
 165 170 175
 Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu
 180 185 190
 Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile
 195 200 205
 Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln
 210 215 220
 Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser
 225 230 235 240
 Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser
 245 250 255
 Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly
 260 265 270
 Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu
 275 280 285
 Pro Ala Ala Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 290 295 300
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 305 310 315 320
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 325 330 335
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 340 345 350

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 355 360 365
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 370 375 380
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 385 390 395 400
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 405 410 415
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 420 425 430
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 435 440 445
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 450 455 460
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 465 470 475 480
 Phe Phe Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 485 490 495
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 500 505 510
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 515 520

<210> 22
 <211> 585
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
 1 5 10 15
 Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
 20 25 30
 Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
 35 40 45
 Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
 50 55 60
 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
 65 70 75 80
 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
 85 90 95
 Tyr Ser Cys Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys
 100 105 110
 Asp Leu Asn Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Ala Ser Arg
 115 120 125

Ala Ala Gly Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val
130 135 140

Val Phe Val Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser
145 150 155 160

Ala Gln Ala Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln
165 170 175

Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr
180 185 190

Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly
195 200 205

Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile
210 215 220

Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro
225 230 235 240

Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe
245 250 255

Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser
260 265 270

Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln
275 280 285

Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala
290 295 300

Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile
305 310 315 320

Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe
325 330 335

Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Ala Ala
340 345 350

Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
355 360 365

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
370 375 380

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
385 390 395 400

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
405 410 415

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
420 425 430

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
435 440 445

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
450 455 460

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 465 470 475 480

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 485 490 495

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 500 505 510

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 515 520 525

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 530 535 540

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 545 550 555 560

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 565 570 575

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 580 585

<210> 23
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 23
 gtacagtggc tgaccactca gaag

24

<210> 24
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Primer

<400> 24
 ggtggactac aagggtgaac agc

23